



SEQUENCE LISTING

<110> ASAKO, HIRONUKI
MATSUMURA, KENJI
SHIMIZU, MASATOSHI
ITO, NOBUYA
WAKITA, RYUHEI

<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE
4-HALO-3-HYDROXYBUTANIC ACID

<130> 12249

<140> US 10/004,115
<141> 2001-12-06

<150> JP 2000-372704
<151> 2000-12-07

<150> JP 2001-006144
<151> 2001-01-15

<150> JP 2001-026594
<151> 2001-02-02

<150> JP 2001-175175
<151> 2001-06-11

<160> 33

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20 25 30
Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
35 40 45
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
50 55 60
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
65 70 75 80
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
85 90 95
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
100 105 110
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
115 120 125
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
130 135 140
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
145 150 155 160
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
165 170 175
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
180 185 190

Glu Ile His Pro Phe Leu Pro Asn Glu Glu Ile Val Gln Tyr Cys Phe
 195 210 205
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220
 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 225 230 235 240
 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255
 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 275 280 285
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
 290 295 300
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 305 310 315 320
 Lys Asn Leu Ser Ala
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<210> 2

<211> 978

<212> DNA

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<221> CDS

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ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc	96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr	
20 25 30	

tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac	144
Tyr Thr Ala Val Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp	
35 40 45	

tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt	192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Ile Arg	
50 55 60	

gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc	240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val	
65 70 75 80	

tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg	288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp	
85 90 95	

tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg	336
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met	
100 105 110	

ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag	384
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	
115 120 125	

ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	

130

135

140

gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag jat Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp 145 150 155 160	460
cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu 165 170 175	528
gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile 180 185 190	576
gag att cac ccc ttc ctg ccz aac gag gag ctg gtg cag tac tgc ttc Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe 195 200 205	624
tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn 210 215 220	672
cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn 225 230 235 240	720
gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc Glu Ile Ala Glu Lys Gly Asn Thr Leu Ala Gln Val Leu Ile Ala 245 250 255	768
tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro 260 265 270	816
aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp 275 280 285	864
ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val 290 295 300	912
aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala 305 310 315 320	960
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Pro

<210> 4

<211> 10
<212> PRT
<213> PENICILLIUM CITRINUM

<400> 4
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<210> 5
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<210> 6
<211> 14
<212> PRT
<213> PENICILLIUM CITRINUM

<400> 6
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<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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OLIGONUCLEOTIDE PRIMER FOR PCR

<400> 8
ggaacytgrt tytgggswacc 20

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<400> 9
tangcnacng gcataaatatt 20

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

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<212> DNA
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<400> 11
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<400> 14
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<210> 15
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 <213> ESCHERICHIA COLI

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 agtqaagggtt ccaaggggcga aacctatnct gctgtcacca ctgcctgaa aaccgggtac 180
 cgtcncttgg actgtgcctg gtactacctg aacaagggtg aggttggta gggtnccgt 240
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 tggaaccacc tccaccgtta tgaggacgtc ctctggtcca ttgacnactc cctgaaggct 360
 cttggacttg actacgttga tatgttccctc gttcaactggc ccattgtgtc cgaaaaaaaaat 420
 ggccagggtg agccaaaaat tggccctgac gccaataacn tcnttctcaa ggacctgacc 480
 gaaanccna ncccacctgg cgcgttatgg aaaaaatttn tgangatccc aaggccaggt 540
 ccattggtgtt ttc当地attgg accattgccc accttgagaa gatgtccaag ttnccaaagg 600
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<210> 16

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<211> 21
<212> DNA
<213> Artificial Sequence

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<212> DNA
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<220>
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<400> 17
caaccagatc gagattcacc 20

<210> 18
<211> 331
<212> DNA
<213> ESCHERICHIA COLI

<400> 18
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cccatcatgt ctaacggaaa gactttcaca ttgagcaacg gctcaagat tcctggcgta 120
ggctttggta ccttcgctag tgaagggtcc aaggcgaga cctatactgc tgtcaccact 180
gccctgaaga ccgggttaccg tcacttggac tgcctgtt actaccta 240
gttggtgagg gtatccgtga cttcctgaag gagaaccctt cggtgaagcg tgaggacatc 300
ttcgtctgca ccaagggtgtg gaaccaccc 331

<210> 19
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<212> DNA
<213> ESCHERICHIA COLI

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cggtgagcgg gtcagcgaga acaagactct gaacgagatc gccgagaagg gcgcaacac 180
ccttgcttag gtttttattt cctgggtct ggcgttgc tacgtcgatc tccccaa 240
ctccaacccc aagcgattt agtccaaactt caagagcatt gagctctccg atgcccactt 300
tgaagccatc aatgcccgtt ccaagggtcg tcacttccgt ttcgtcaaca tgaaggatac 360
tttcggatat gatgtctggc ccgaggagac cgccaaagaa ctgtctcgta gaatcttac 420
gaaattataa aatnacaccn acnaaaancc aaagcgaaat gatgatncc aaaantttt 480
agggtttctt ggtgaaaac gtttattttt cccgaanttga angaatatg gancttgatt 540
tctccaaaaa aaaaaaaaaa aaaaacggtc cgccggccgt ccnnnggggg gcccgggttcc 600
caattcnccc cttatnattt aattctttt taanggggnc aaattccncc nnatttccnt 660
cnaatttgn nggccgcctc caaacttccn tcntnaaagg gncccaattc ccccccatt 720
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42237 DESCRIPTION OF ARTIFICIAL SEQUENCE: DESIGNED OLIGONUCLEOTIDE PRIMERS FOR PCR

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<210> 21
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<213> Artificial Sequence

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<400> 21
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<210> 22
<211> 417
<212> DNA
<213> ESCHERICHIA COLI

<400> 22
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agaagaatgg ccagggttag cccaaagattt gcccgtacgg caaatacgtc atttctcaagg 180
acctgaccggaa gaaaccccgag cccacatggc gcgctatggta gaagattttat gaggatcgca 240
aggccaggta cattgggttc tccaaactggc ccattgcccga ctttgagaag atgtccaagt 300
tcgccaaggat catgcctcac gccaaccaga tcgagattca ccccttcctt cccaaacggagg 360
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<210> 23
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 23
gccccatggctta tgtcttaacgg aaagact 27

<210> 24
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
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<400> 24
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<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: DESIGNED

OLIGONUCLEOTIDE PRIMER FOR PCR

<400> 25
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<210> 26
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 26
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<210> 27
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 <213> ESCHERICHIA COLI

<220>
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 <222> (1)...(786)

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acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct 96
 Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
 20 25 30

aaa gta gtt gtg aac tat cgt tcg aaa gaa gaa gct aac agc gtt 144
 Lys Val Val Asn Tyr Arg Ser Lys Glu Glu Ala Asn Ser Val
 35 40 45

tta gaa gaa att aaa aaa gtg ggc gga gag gct att gcc gtc aaa ggt 192
 Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly
 50 55 60

gat gta aca gtt gag tct gat gtg atc aat tta gttcaa tct gct att 240
 Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile
 65 70 75 80

aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa 288
 Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu
 85 90 95

aat ccg gtt tcg tct cat gaa atg tct tta agt gat tgg aat aaa gtc 336
 Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
 100 105 110

att gat acg aac tta acg gga gca ttt tta ggc agc cgt gaa gcg att 384
 Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
 115 120 125

aaa tat ttt gtg gaa aat gat att aag gga aca gtt att aac atg tcg 432
 Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser
 130 135 140

agt gtt tac ggg aaa att cct tgg cca tta ttt gtt cat tac gca gca	480
Ser Val Asn Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	
145 150 155 160	
agt Raa ggt gga atg tgg ctc atg ac' gaa aca ctt gca tta gaa tat	519
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	
165 170 175	
gct cca aaa ggt att cgt gta aat aac att gga ccg gga gcg att att	576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	
180 185 190	
aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat	624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp	
195 200 205	
gta gaa agc atg att cca atg gga tac att gga gag ccg gaa gaa att	672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	
210 215 220	
gca gcg gtt gct gca tgg cta gct tct tca gag gca agt tat gta aca	720
Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr	
225 230 235 240	
ggg att aca ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc	768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe	
245 250 255	
caa gca gga cgc gga taa	786
Gln Ala Gly Arg Gly *	
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ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc	96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr	
20 25 30	
tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac	144
Tyr Thr Ala Val Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp	
35 40 45	
tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt	192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg	
50 55 60	
gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc	240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val	
65 70 75 80	

tgc acc aag gtc tgg aac cac ctc cac cgt tat gag gag gtc ctc tgg Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp 85 90 95	288
tcc att gag gag tcc ctt aag cgt ctt ggc ctt gag tac gtt gat att Ser Ile Asp Asp Ser Ile Lys Arg Leu Gly Leu Asp Tyr Val Asp Met 100 105 110	336
tcc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu 115 120 125	384
ccc aag att ggc ctt gag ggc aaa tac gtc att ctc aag gac ctg acc Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr 130 135 140	432
gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp 145 150 155 160	480
cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu 165 170 175	528
gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile 180 185 190	576
gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe 195 200 205	624
tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn 210 215 220	672
cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn 225 230 235 240	720
gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala 245 250 255	768
tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro 260 265 270	816
aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp 275 280 285	864
ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val 290 295 300	912
aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala 305 310 315 320	960
aag aac ctg tct gcg tga atctctacga aattataa Lys Asn Leu Ser Ala *	996
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<210> 29

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<212> DNA

<213> Artificial Sequence

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE DESIGNED
OLIGONUCLEOTIDE PRIMER FOR PCR

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cggatccgtt cacgcagaca ggttcttgg

29

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<211> 27

<212> DNA

<213> Artificial Sequence

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE DESIGNED
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<212> DNA

<213> Artificial Sequence

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE DESIGNED
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<400> 32

cggatccgtt atccgcgtcc tgc

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<211> 28

<212> DNA

<213> Artificial Sequence

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE DESIGNED
OLIGONUCLEOTIDE PRIMER FOR PCR

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<212> PRT

<213> CORYNEBACTERIUM SP.

<400> 34

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Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
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Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly

<210> 35
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<212> DNA
<213> CORYNEBACTERIUM SP.

<220>
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<222> (1) . . . (1158)

<400> 35

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48

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gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc
Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
          20           25           30

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96

acc gct gct ggc gtc tac cac tgg gag gag ttc atc atg agg cta ccc

144

Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
 35 40 45

gaa gag cag tac acc tac ggc ctt ccc atc acg ctc ggt cac gaa ggc 192
 Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Gln Glu
 50 55 60

gca ggc aag gtc gcc gcc gtc ggc gag ggt gtc gaa ggt ctc gac atc 240
 Ala Gly Lys Val Ala Ala Val Gly Gln Gly Val Glu Gly Leu Asp Ile
 65 70 75 80

gga acc aat gtc gtc gtc tac ggg oct tag get tgc ggc aac tgt tgg 288
 Gly Thr Asn Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
 85 90 95

cac tgc tca caa gga ctc gag aac tat tgc tct cgc gcc caa gaa ctc 336
 His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
 100 105 110

gga atc aat cct ccc ggt ctc ggt gca ccc ggc gcg ttg gcc gag ttc 384
 Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
 115 120 125

atg atc gtc gat tct cct cgc cac ctt gtc ccg atc ggt gac ctc gac 432
 Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
 130 135 140

ccg gtc aag acg gtg ccg ctg acc gac gcc ggt ctg acg ccg tat cac 480
 Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
 145 150 155 160

gcg atc aag cgt tct ctg ccg aaa ctt cgc gga ggc tcg tac gcg gtt 528
 Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
 165 170 175

gtc att ggt acc ggc ggt ctc ggc cac gtc gct att cag ctc ctc cgc 576
 Val Ile Gly Thr Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
 180 185 190

cac ctc tcg gca acg gtc atc gct ttg gac gtg agc gcg gac aag 624
 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
 195 200 205

ctc gaa ctg gca acc aag gta ggc gct cac gaa gtg gtt ctg tcc gac 672
 Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
 210 215 220

aag gac gcg gcc gag aac gtc cgc aag atc act gga agt caa ggc gcc 720
 Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
 225 230 235 240

gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg 768
 Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
 245 250 255

atg gct gtc gcc ggc gtc gga tca gac gtc acg atc gtc ggg atc ggg 816
 Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
 260 265 270

gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag 864
 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
 275 280 285

.gtt tgg gtg aca gtt ccg tat tgg ggt gcc cgc aac gag tgg atc gaa	912
Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu	
290	295
	300
ttg att gag ctc gca gac gct ggc atc ttc gag atc ggt gat cgt gag	961
Ieu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Gly Asp	
305	310
	315
	320
cct cag tct cga caa cgg tgc cga aac gta tcg acg act ggc tgg cgg	1008
Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg	
325	330
	335
aac gct cag cgg cgg tgc ggt tgg tct gta gta ccc asa	1056
Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr	
340	345
	350
gcg gta gaa cga cag cgg aaa aac act gat gcc cgg ccc aat tcg att	1104
Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile	
355	360
	365
cgg ccg ggc atc agt gtc aga aat tcg gtg tgc gct agc tgc acg cct	1152
Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro	
370	375
	380
cga tga	1158
Arg *	
385	